IN THE CLAIMS

Claim 1 (canceled)

2. (currently amended) A method for identifying the species or subspecies of a mycobacterial strain comprising the steps of:

a) digesting a DNA fragment which has a sequence selected from the group consisting SEQ ID NO:1 to SEQ ID NO:24 with at least one restriction enzyme selected from the group consisting of *Hae*III, *Msp*I, *Sau*3AI, and *Bst*EII to obtain a first DNA fragment length polymorphism pattern;

b) isolating a DNA fragment from the mycobacterial strain to be identified;

c) amplifying rpoB region of the DNA fragment isolated in step (b), said amplification being performed by using a primer of SEQ ID NO:25 [15] or SEQ ID NO:26 to produce an amplified DNA fragment;

d) digesting the amplified DNA fragment of [amplified in] step c) with the at least one restriction enzyme employed in step a) to obtain a second DNA fragment length polymorphism pattern; and

e) comparing the first DNA fragment length polymorphism pattern obtained in step a) with the second DNA fragment length polymorphism pattern obtained in step d), thereby identifying the species or subspecies of a mycobacterial strain.

3. (currently amended) A method of claim 2, wherein said first and second DNA fragment length polymorphism patterns are obtained by electrophoresis.

Claim 4 (canceled)

5. (previously amended) A method of claim 2, wherein said mycobacterial strain is selected from the group consisting of *M. tuberculosis, M. avium, M. abscessus, M. flavescens, M. africanum, M. bovis, M. chelonae, M. celatum, M. fortuitum, M.*

gordonae, M. gastri, M. haemophilum, M. intracellulare, M. kansasii, M. malmoense, M. marinum, M. szulgai, M. terrae, M. scrojulaceum, M. ulcerans, and *M. xenopi.*